



QY 121 TGGGCAAGAGGAGAGGAGTTCTGCTGCGGCTGGTGGATTCGACATGATCTTGTAAC 180  
 |||||  
 Db 121 TGGGGCAAGAGGAGAGGAGTTCTGCTGCGGCTGGTGGATTCGACATGATCTTGTAAC 180  
 QY 181 GTGTGGCGATTCCTCTACATCTGTAAACGAATGAGGCGGTGCTCTGATCCGTAC 240  
 |||||  
 Db 181 GTGTGGCGATTCCTCTACATCTGTAAACGAATGAGGCGGTGCTCTGATCCGTAC 240  
 QY 241 TGGGTAATGCTGCTGTTGGGCGGCGGCGGCTGTTCTTCTGGAACCTGGGCGGCGGCG 300  
 |||||  
 Db 241 TGGGTAATGCTGCTGTTGGGCGGCGGCGGCTGTTCTTCTGGAACCTGGGCGGCGGCG 300  
 QY 301 TACACACGCTGGGCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 |||||  
 Db 301 TACACACGCTGGGCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 QY 361 GGGTATGCGCATCTGCAATGATCGACATCTACATGCGGATGATGATGATGATGATGATGAT 420  
 |||||  
 Db 361 GGGTATGCGCATCTGCAATGATCGACATCTACATGCGGATGATGATGATGATGATGATGAT 420  
 QY 421 TGGGCGGTGATTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 |||||  
 Db 421 TGGGCGGTGATTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 QY 481 AGCTGCGACAGAGTGGAAACAGCGCTGTGACAGCGGCTGACCTGACCTGACCTGATAT 540  
 |||||  
 Db 481 AGCTGCGACAGAGTGGAAACAGCGCTGTGACAGCGGCTGACCTGACCTGACCTGATAT 540  
 QY 541 CCTAATCTTCTTACACCGGCGGAGAGTCTTCTGAAAGCTAATGATGATGAGAGAGCAAG 600  
 |||||  
 Db 541 CCTAATCTTCTTACACCGGCGGAGAGTCTTCTGAAAGCTAATGATGATGAGAGAGCAAG 600  
 QY 601 TCTAAGCGGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 |||||  
 Db 601 TCTAAGCGGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 QY 661 GTCTTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 |||||  
 Db 661 GTCTTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 QY 721 TGGGTGACAGCTCTGCGGCGGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 |||||  
 Db 721 TGGGTGACAGCTCTGCGGCGGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 QY 781 CTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 |||||  
 Db 781 CTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 QY 841 AACTCTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 |||||  
 Db 841 AACTCTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 QY 901 GGAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 |||||  
 Db 901 GGAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 QY 961 CTTCATCT 1020  
 |||||  
 Db 961 CTTCATCT 1020  
 QY 1021 GTTTTGGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
 |||||  
 Db 1021 GTTTTGGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
 QY 1081 CCGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 |||||  
 Db 1081 CCGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 QY 1141 TGGGCGCATATCT 1200  
 |||||  
 Db 1141 TGGGCGCATATCT 1200  
 QY 1201 GTTGAAGGAGTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
 |||||

Db 1201 GTTGAAGGAGTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
 QY 1261 GAAGTATTTGGGCTGTACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 |||||  
 Db 1261 GAAGTATTTGGGCTGTACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 QY 1321 TACGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 |||||  
 Db 1321 TACGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 QY 1381 TTGCT 1440  
 |||||  
 Db 1381 TTGCT 1440  
 QY 1441 GAAGATGTAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 |||||  
 Db 1441 GAAGATGTAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 QY 1501 TACATGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
 |||||  
 Db 1501 TACATGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
 QY 1561 ATGCTGCGGCGGGAATACACCTATCCCTGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
 |||||  
 Db 1561 ATGCTGCGGCGGGAATACACCTATCCCTGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
 QY 1621 GGCACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
 |||||  
 Db 1621 GGCACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
 QY 1681 AATTCATCAACCGCATCAAGCAATCAACCTCCGGAAGTACGATGATGATGATGATGATGATGAT 1740  
 |||||  
 Db 1681 AATTCATCAACCGCATCAAGCAATCAACCTCCGGAAGTACGATGATGATGATGATGATGATGAT 1740  
 QY 1741 GACTTACCTTATGCAACTGTGA 1764  
 |||||  
 Db 1741 GACTTACCTTATGCAACTGTGA 1764  
 RESULT 2  
 US-10-144-771-11577  
 ; Sequence 11577, Application US/10144771  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig  
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
 ; FILE REFERENCE: C1001321  
 ; CURRENT APPLICATION NUMBER: US/10/144,771  
 ; CURRENT FILING DATE: 2002-05-15  
 ; NUMBER OF SEQ ID NOS: 47235  
 ; SEQ ID NO 11577  
 ; LENGTH: 2745  
 ; TYPE: DNA  
 ; ORGANISM: HUMAN  
 US-10-144-771-11577  
 Query Match 32.9%; Score 579.8; DB 14; Length 2745;  
 Best Local Similarity 59.8%; Pred. No. 1.2e-165;  
 Matches 989; Conservative 0; Mismatches 662; Indels 3; Gaps 1;

Db	577	TCGCCGCTTCTACATGAGAGCTGCACCCCTGGGCCAGTACACCGAAATGGGTGCATTTCTA	636
OY	326	TTGCGAAACGATGTGCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA	385
Db	637	TATGAGAGAGATGTGCCCGCATTTTCAAAAGGCAATGGCTATGCCATCTGCATCATTTGGCT	696
OY	386	TCTCATGGGCGATCTACTACAAACAGATCATCGGATGGGGGGGTATTAATTCGTT	445
Db	697	TTTATATCGCCTCTACTATACACCATCATATAGCCTGGGCGCTTACTACTCATCTTCT	756
OY	446	CTCTGGCGTCTATTAACCTGTGTGCTGCCATGAGCCAGCTGCGACACGATGGAACACGC	505
Db	757	CCTTACAGGACACACTGCGCCCTGGACACAGCTGCAGAACTTTGAAACACTGGAACCTCA	816
OY	506	CGCGTGCAGCCCGGCTCACCTCACCCTCAGACTAATTCCTAATCTTTTACACCCGGCAAGG	565
Db	817	CCAACTACTTCGCCGAGGACAAATCACCTGGACATCTCATTTCCACGTCACCTCTCGAGG	876
OY	566	AGTTCTTCGAAAGTATATGTATTTGGAGCAGCACAAGTCAACGGCGCTGATACATGGGGC	625
Db	877	AGTTTACTCTCGGCATGTCTCTGGAGATCATCATGTAACAAAGGACTCCAGGACCTGGGGA	936
OY	626	CGATCAAGCCCTCGCTGCGTCTGTGTGTGTGTGTGGGGCTTTTGTCTCTACTTCTCT	685
Db	937	CCATACAGTGCACACTGGCTCTCTGTCATCATGATCATCTTACCATATTATCTACTACACA	996
OY	686	TGTTGAAAGAGTAGAGAGTCTGCGCAAGTGGTGGGTGACAGCTGTGCCCCGTACG	745
Db	997	TCTGGAAGAGGTCAAAACGTCTGGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1056
OY	746	TGTGTGCTGCTGATTTCTGCTGGCGAGAGGCGTACGCTTTCAGAGACGAGGAGGCATAC	805
Db	1057	TTTGCTCTTTCGTCTGCTGCTGGTGGAGGGAGCCACTTTCGAGAGCCGGAGAGGGGCTTG	1116
OY	806	GCTACTACCTTACCACAGAGTGGGACAAATTTGCAAAACTCTAAGGTATGATTTGACCGGG	865
Db	1117	TCTTTTACTTAAACCACACTGGACGAAGAACTCTTGGAGACAGGGGTGTGGGTGTGATGCTG	1176
OY	866	CATCCAGATTTTCTCTGCTGCTGCGTCCGGGTTTCGGAACCTTACTGCGCTCTCCACCT	925
Db	1177	CGGCTCAGATCTTTTCTCTCTCTGTGGCCCGGGGTTTGGGCTTCTCTGCGTTTGGTACT	1236
OY	926	ACACACAGTTCAACAACACTGCTACAGGAGCGGCTATATCTTCTTCTATCAACTGCT	985
Db	1237	ACAACAGTTCAACAACACTGTTTACCAAGATGCCCTGTGACCAAGTGTGTGAACCTGCA	1296
OY	986	TGACACAGTCTCTGTGCTGTTTGCATATTTCTCGGTTTGGGGTACATGGCGACGCTTC	1045
Db	1297	TGACAGGTTTGTCTGTGCTTGTGTCTCTACGCTCTTGGCTACATGGCTGATGATGA	1356
OY	1046	AGAACAGAGCAT--CGAGGAGTTGGCTTCGAAGGCCCTGAGCTGGTGTTCATCGTGT	1102
Db	1357	GGAAAGAAAGACGTGTCCGAGGTGGCCAAAGACGGGGGCCACAGCTCTCTTTTATCATCAT	1416
OY	1103	ACCCGAGGCGATGCGCACCATGACAGCCGCTCGGTTTGTGGGCATCATCTTTTCCGCA	1166
Db	1417	ATGCGGAGGCAATAGCTACATGCGCAGCATCAATTTTGGCCATCATCTTTTCTCTCA	1476
OY	1163	TGCTTATTTACCTGGGACTGACAGTATTTTGGAGGCTTGGAGCACTCACACGCGCTC	1222
Db	1477	TGTTAATCACCTGGGTTTGGATAGTACGTTTTCAGGCTCGTGAAGGTGTGATCACAGCTG	1536
OY	1223	TTTGGAGCAATATCTCTCGAGTGTTAGGCAACATCGGAAGTATTTGTGGCTGTACTGC	1288
Db	1537	TGTTGGATGAGATTTCTCTACATCTGGGCGCAAGCGAGGAAATGGTTTGTCTCATCTGGG	1596
OY	1283	TTTCTTTCATATATTTTGGCGCTGCGCCACACACATPATGGTGGTATTAATCTCGTAG	1342
Db	1597	TCATCAGTGGATCTTGGGATCCCTGCTCACACTGACATTCAGAGAGGGCGTATGTGTGA	1656
OY	1343	ACCTACTCAATGTGTATGGCCCTGGATTTGCGATTTATCTGTGGTATTTTCTGAGGCTG	1402

QY	Db	Sequence	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
QY	1657	CCCGCTGGAAGATGACGCCACGGCGCCACAGAGTCTACATGAGGCTTCATGAGGCGC	32.88	15	3190	60.0%	1.7e-155	0	651	3
QY	1403	CCGGCTGTGCTGGGCTATATGCCCTGCACCGGTTCTTGAAGATGTAGACCATCTGG	32.88	15	3190	60.0%	1.7e-155	0	651	3
Db	1717	TCGTCGCTGTGGTTCATATGAAATCTACTAGTTCTACCGACGACGTAAAGAAATCTGG	32.88	15	3190	60.0%	1.7e-155	0	651	3
QY	1463	GGCACCACCCCGATGGTCTGGAGGACGCTGGTGGTTCATACATAGTCCGATATCTGG	32.88	15	3190	60.0%	1.7e-155	0	651	3
Db	1777	GCTTCACGCCCCGGATGGTTTGGAGGATCTCTGAGGAGTCTATCATGCTCTCTTTTCC	32.88	15	3190	60.0%	1.7e-155	0	651	3
QY	1523	TGTCGCTGTTCGTTCTCCGTTCTGACACGAGAGATGCTGGCGGGAATATACCT	32.88	15	3190	60.0%	1.7e-155	0	651	3
Db	1837	TGTCATCATATTTGACGATTTTTCATGATGATGCACCCCAACCTCCGCTTTTCCATATACAT	32.88	15	3190	60.0%	1.7e-155	0	651	3
QY	1583	ATCCCTCATGCTCATACCGTACGCTGGGATGAGACCGGACACCGCTCTCGTGCATTC	32.88	15	3190	60.0%	1.7e-155	0	651	3
Db	1897	ATCCCACTGAGATATATCTTGGCTATCTGATCATGAGAACATGCTCTGATATCTGATCC	32.88	15	3190	60.0%	1.7e-155	0	651	3
QY	1643	CTCTTTCATATATCTACAACTGCTCATCTCTCGGCAATTTGCATACACCGATCAGA	32.88	15	3190	60.0%	1.7e-155	0	651	3
Db	1957	CTATATATCATATTTATTCGGCTGATACGACTCGAGGACACTTAAGAGCGCATTTATTA	32.88	15	3190	60.0%	1.7e-155	0	651	3
QY	1703	CAATCAACGTCGGAAGTGCATCTACCTC	32.88	15	3190	60.0%	1.7e-155	0	651	3
Db	2017	AAAGTATCATCTCTGAAACACCAACGGAATTTCC	32.88	15	3190	60.0%	1.7e-155	0	651	3
RESULT 3										
US-10-219-051B-13968										
Sequence 13968, Application US/10219051B										
GENERAL INFORMATION:										
APPLICANT: The General Hospital Corporation doing business as Massachusetts General										
APPLICANT: Hospital / Bayer AG										
TITLE OF INVENTION: Nucleotide sequences involved in pain										
FILE REFERENCE: Lea 35693 Foreign Countries										
CURRENT APPLICATION NUMBER: US/10/219,051B										
CURRENT FILING DATE: 2003-05-09										
PRIOR APPLICATION NUMBER: US 60/312,147										
PRIOR FILING DATE: 2001-08-14										
PRIOR APPLICATION NUMBER: US 60/346,382										
PRIOR FILING DATE: 2001-11-01										
PRIOR APPLICATION NUMBER: US 60/333,347										
PRIOR FILING DATE: 2001-11-26										
NUMBER OF SEQ ID NOS: 14715										
SOFTWARE: Perl script										

OY	326	TCGTGAAACGATGTGGCCCGCCGCTTAAAGGTGTCGCTATGCGCATGTGCATGATGCACA	385
Db	609	TATGGAGAGATCTGCCCCGATTTTCAAGGCATTGGTTAGCCATCTGCAATCGCTT	668
OY	386	TCATCATGGGATGTACTACAACAGATCGATGGAGTGGCGGTATTAATACCTGATCGCTT	445
Db	669	TTTACATGCGCTCTACTACAACACATCATAGCCTGGCGCTGTACTACCTCATCTCTCT	728
OY	446	CTTCGCGTCTATAACTCTGTGCTGGCATGGACCACTGGGACACAGATGGAAACAGC	505
Db	729	CCCTACGGAGACCGGCTGCCCTGGACACTGTACAGTAATCTCTGGAAACCTGGCAACTGCA	788
OY	506	CGCTGTGCACCGGGTCACTCCACCTCAGATTAATCCATCTTTCTACACGGCGGAAG	565
Db	789	CCAATCTACTTGGCCGAGGAAACAATCATCTGGACGTGTCATTTCCACGTCGCCCGCTAGG	848
OY	566	AGTTCTTGGAACGTAATGTATTGGAGCAGCAAGTCTACACGCCCTGGATACATGGGCG	625
Db	849	AGTTCTACTTGGCCATCTCTCTGGAGATCAACAGTCTTAAAGGATCCAGAGCTGGGCA	908
OY	626	CGATCAAGCCCTCCCTGGCTGTGTGTGTGTGGGGTCTTGTCTCTGCTACTTCTCTCT	685
Db	909	CCATTCAGCTGGCAGCTGACTCTCTGTGCATCGTGTCTATCTTACCGTATCTACTTTAGCA	968
OY	686	TGTGGAAAGAGTCAAGAGCTGTGGCAAGGTGTGTGTGGGTGACAGCTCTGGCCCCGTAG	745
Db	969	TCTGGAAAGGCGTCAAAAACATCTGGCAAGGTGTGTGGGTGACAGCCACTTCCCATACA	1028
OY	746	TGGTGTCTGATTTCTGTGTGGCAGAGGCGTCACAGCTTCACAGAGCGACGGAGGGCAATAC	805
Db	1029	TTGTGCTCTCTGTCTGTCTGTGTGGAGGGGGGCCACCCCTTCTGTGAACCTGTGGAGGGGTG	1088
OY	806	GCTACTACTTACCCACAGAGTGGCAACAATTCGAAAACCTCTAAGTATGATGTAGCGGG	865
Db	1089	TCTTCTACTTGAAAACCAACTGTGGCAAAACTCTTGGAGACAGGGGTGTGGGTACATGGCG	1148
OY	866	CATCCGAGATTTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	925
Db	1149	CCGCTCAGATCTTCTCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	1208
OY	926	ACAACAGATTTCACAACTGCTACACAGGAGCGGCTCATCTCTCTCATCAACTGCT	985
Db	1209	ACAACAGATTTCACAACTGCTACACAGGAGCGGCTCATCTCTCTCATCAACTGCT	1268
OY	986	TGACCAAGTTCCTGT	1045
Db	1269	TGACCAAGTTCCTGT	1328
OY	1046	AGAACAGAGCATGAGAGGAGTGTAGC--CTGAAAGGCGCTGAGACTGGTGTTCATCGGT	1102
Db	1329	GGATGGAAGATGTGTGAGAGGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1388
OY	1103	ACCCGAGGCGATGCGCACATGACCGGCTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1162
Db	1389	ATGCAAGAGGCGATGCGCACATGACCGGCTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1448
OY	1163	TGCTTATTAACCGTGGAGTGTGAGTACTTTTGGAGGCTTGGAGGAGTGTGAGGAGTGTGAGGAG	1222
Db	1449	TGTTAATACCGTGGAGTGTGAGTACTTTTGGAGGCTTGGAGGAGTGTGAGGAGTGTGAGGAG	1508
OY	1223	TTTGCAGAGATATCTCTGAGTGTTAGGAGAGACATCCGAAGTATTTGTGGCTGTACTGCG	1282
Db	1509	TGCTGAGATGATCTCTCTGAGTGTTAGGAGAGACATCCGAAGTATTTGTGGCTGTACTGCG	1568
OY	1283	TTTGTGTCATCTAATTTTGGCGTCTGTGCCACACACATACATGAGTGTGTATACCTCTGTAG	1342
Db	1569	TCATTCAGGTGTGTGTGGAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1628
OY	1343	ACCTACGATATGTATGAGCGCGTGGATTTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1402
Db	1629	CTCTGCTGTGAGAGTATATCCACGGGGCGAGAGTGTCTACCGTGTGGCCCTCATTCAGGCGG	1688

Oy	1403	CCGGCGGTGGTGGGGTGTATGAGCGGCACGCGTTCCTCTGAAGATGTGAGSACATATGCGG	1462
Db	1689	TGCGCGTCTTGGTCTTATGGAATCACTCAgTTCTTGACGAGATGTGAAGAGATGCGG	1748
Oy	1463	GGCACACCCCTGAGATGGTTCTGAGAGACCTTGGTCTTACATAGTCCGCTATTCTTGC	1522
Db	1749	GCTTCAGCGCCGGGATGTTTGTGGAGATCTCTGGGTGGCCATCAGCCCTCTGTTTCTCC	1808
Oy	1523	TGTGCTGTTCGTTCTTCCGTTCTTGGCACAGAGAGATGCTGGCGGGGAATACACCT	1582
Db	1809	TGTTTCATCATTTGCAAGTTTCTGTGATGAGCCACCACCCAGCTACGGGTTTTCATATACAAC	1868
Oy	1583	ATCCCTCATGCTCATACCCGTAGGCTGGGTGATGATACCGGCACACCGCTCTGCTGATTC	1642
Db	1869	ATCCCACTGAGAGATCGTCTTGGGCTACTGCATAGAGGATTCGTCCTCATCTGCAATCC	1928
Oy	1643	CTCTTTCATATATACAAACTGCTCATCATCTCTGGCAATTGCATCAACCGCATCAAGA	1702
Db	1929	CTACCTATATCATTTATTCGCTGTGATACGACACTCCGGGGACACTTAAGAGGCGCATTTATTA	1988
Oy	1703	CAATCCAACGTCGCGAA	1719
Db	1989	AAAGTATCATCTCTGAA	2005

```

RESULT 4
US-60-453-135-5294
; Sequence 5294, Application, US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01456
; CURRENT APPLICATION NUMBER: US/60/453,135
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5294
; LENGTH: 2964
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-5294

Query Match          31.5%; Score 554.8; DB 18; Length 2964;
Best Local Similarity 59.5%; Pred. No. 5,3e-158;
Matches 953; Conservative 2; Mismatches 644; Indels 3; Gaps 1;

OY 107 GGCACGCCGACAGCTGTGGCGAAGAGCAGAGCTTCTGTGCGGCTGTGGATTCGCAG 166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 GGGACGGGGAACCTGTGGGCAAGAGGTGGATTCTTCTTCACAGATTGGCTATAGCG 361

OY 167 TGGATCTTGTGAACGTGTGGGATTCCTCCATCATCTGTTACAGAAATGGAGCGGTGGCT 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 TGGACCTGTGGCAATGTCTGTGGCGTTCCCTTACATATGTTACAGAAATGGAGGGGGCAT 421

OY 227 TCTCGATCCCTACTGCGCTTATGTGCTGCTTTGGCGGGGCTGCGCTGTCTCTCTGGAAC 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 TCTCTCTCCCTACACATCATATGGCCATTTTGGGGGAATCCCGCTTTTACATAGGAGC 481

OY 287 TGGCGGCTGTGGCCAGTACCAAGCGGTGGGCTGCTCTACTCTCTTGGAAACGATGTGCCCCG 346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 TCGGCACTGTGGACAGTACCCAGCAAAATGGATGATTTCAATATAGGAGGAAATACTGCCGA 541

OY 347 CGCTTAAAGGTGTGGGCTATGTCATCTGCATGATGACATACATACATAGGCAATGTACTACA 406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 TTTTCAAGGATTTGGTTATGCTCATCTGCATCATATGGCTTTTACATATGCTTCTACTACA 601

OY 407 ACAGATCATGAGATGGCGGCTGTATTACCTGATGCGTTCTCCGCTCTATAAAGCTGTG 466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 602 ACACATCATATGGCGGCTGTATACCTATACCTCATATCTCTCTTACAGGACCAAGTGGCCCT 661

OY 467 TGTGTCCATGTAGCAAGCTGTGCACAAAGATGGAAACAGCGCGCTGTGACAGCCGTTACCT 526

```

Db 662 GGACACAGCTGCASAACTCTGGAACACTGGCAACTGCACCAATTAATCTTCCGAGACA 721  
Qy 527 CACCTCAGACTAATTCCTACTCTTCTACACGGCGCAAGAGTCTTCAGACTATGAT 586  
Db 722 ACATCACCCTGAGACCTCCATTCCACGCTCCCTGCGAAGAAATTTTACAGCGCCACGTC 781  
Qy 587 TGGAGCAGCACAAGTCTAAGCGCTGATGATGACATGGGCGCCATCAAGCGCTGCGTC 646  
Db 782 TGCAGATTCACCGGCTTAAGGGGCTCCAGGACCTGGGGGCGATCGCGGACGTCGCC 841  
Qy 647 TGTGTGTCTGGGGCTCTTTGTCTCTGCTACTCTCTTGTGAAAGAGTCAAGAGTG 706  
Db 842 TCTGCATCATCTGATCTTCACTGTTATCTTACTTACATCTGGAAGGCGCAAGACT 901  
Qy 707 CTGGCAAGGTGGTGGGTGACAGCTCGGCCCTAGCTGCTGCTGATCTGCTGG 766  
Db 902 CTGGCAAGGTGGTGGGTGACAGCTCTTCCCTAATATCATCTCTTCTGCTGCTGG 961  
Qy 767 CGAGAGCGCTCAGCTTCCAGGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 826  
Db 962 TGAGGGGAGTCAACCTCCCTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1021  
Qy 827 GGCACAAATTCGAAATCTTAAGGATGATGATGACGCGGATCCAGATTTTCTTCTGC 886  
Db 1022 GGCAGAAATCTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1081  
Qy 887 TCGGTCGGGGTGGAGACCTACTGAGGCTCCAGCTACACAAAGTTCACAAACACT 946  
Db 1082 TTGGTCCGGGCTTGGGGTCTCGCTGCTTGTGAGTACACAAAGTTCACAAACACT 1141  
Qy 947 GCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1006  
Db 1142 GCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1201  
Qy 1007 TCGTCAATTTCTCGGTTTGGGGATACATGGCGGAGCTTCAAGAGGAGGAGGAGG 1066  
Db 1202 TTGTCAATTTCTCGGTTTGGGGATACATGGCGGAGGAGGAGGAGGAGGAGGAGG 1261  
Qy 1067 TTGGC --- CTGGAAGGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1123  
Db 1262 TGGCCAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1321  
Qy 1124 TGACCGGCTCGGTTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1183  
Db 1322 TGCCAGGCTCCACTTTCTTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1381  
Qy 1184 ACAGTACTTTTGGAGGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1243  
Db 1382 ACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1441  
Qy 1244 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1303  
Db 1442 TCTGGGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1501  
Qy 1304 CTCTGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1363  
Db 1502 CCGTGGTCAACCTCTTTTGAAGGGGCTCAGTGTGAAGAGGAGGAGGAGGAGGAGGAGG 1561  
Qy 1364 CTGGAATTTGGGAGGCTTATCTGATTTGCTGAGGAGGAGGAGGAGGAGGAGGAGG 1423  
Db 1562 CGGGGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1621  
Qy 1424 GCGTGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1483  
Db 1622 GCATCACTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1681  
Qy 1484 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1543  
Db 1682 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1741  
Qy 1544 TTCTGGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1603

Db 1742 TGATGAGCCCGCAGACACTAGACTTTTCCAAATATATATATATATATATATATAT 1801  
Qy 1604 TAGGCTGGGTATGAGCCGGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1663  
Db 1802 TGGGTTACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1861  
Qy 1664 TGCATCATCTCTGCAATTTGATCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1705  
Db 1862 TGATCATCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1903  
  
RESULT 5  
US-60-453-050-5294  
; Sequence 5294, Application us/60453050  
; GENERAL INFORMATION:  
; APPLICANT: CARLILL, Michele  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 82/62  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 5294  
; LENGTH: 2964  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-453-050-5294  
  
Query Match 31.5%; Score 554.8; DB 18; Length 2964;  
Best Local Similarity 59.5%; Pred. No. 5.3e-158;  
Matches 953; Conservative 2; Mismatches 644; Indels 3; Gaps 1;  
  
Qy 107 GGCAGCGGAGACCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 166  
Db 302 GGGAGCGGAGACCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 361  
Qy 167 TGAGTCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 226  
Db 362 TGGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 421  
Qy 227 TCCATGATCCGCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 286  
Db 422 TCCCTCTCCCTACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 481  
Qy 287 TGGCGCTGGGCGAGTACACGCGCTGCGCTGCTGCTGGAAGGAGGAGGAGGAGGAGG 346  
Db 482 TCGCACTGGGAGACAGTACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 541  
Qy 347 CGCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 406  
Db 542 TTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 601  
Qy 407 ACAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 466  
Db 602 ACAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 661  
Qy 467 TGTGCGCATGAGCAGGCTGCGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 526  
Db 662 GGAGCAGGCTGCAASAACTCTGGAACACTGGACAGCAAAATTAATCTTCCGAGGACA 721  
Qy 527 CACCTCAGACTAATCTTAATCTTCTTACACCGGCAAGAGGAGGAGGAGGAGGAGGAGGAGG 586  
Db 722 ACATCACCCTGAGCCTCCATTCCACGCTCCCTGCGAAGAAATTTTACAGCGCCACGTC 781  
Qy 587 TGGAGCAGCACAAGTCTAAGCGCTGATGATGACATGGGCGCCATCAAGCGCTGCGTC 646  
Db 782 TGCAGATTCACCGGCTTAAGGGGCTCCAGGACCTGGGGGCGATCGCGGACGTCGCC 841  
Qy 647 TGTGTGTCTGGGGCTTTTGTCTGCTGCTACTCTCTTGTGGAAGAGTCAAGAGTG 706  
Db 842 TCTGCATCATCTGATCTTCACTGTTATCTTACTTACGATCTGGAAGGCGTCAAGACT 901



Db	1082	TTGGTCCGGGCTTTGGGGTCCCTGCTGGCTTTTGCTACTACACAAAGTTTCACAACT	1141
QY	947	GCTACAGGAGCGGCTCATCACTCTTCTTATCAACATCGCTTGACAGCTTCTTGCTG	1006
Db	1142	GCTACCAAGATCCCCCTGGTGACACGAGCGTGATCAACTCATATGACAGAGCTTCCTTCGGGAT	1201
QY	1007	TGCTATTTTTCGGGTTTGGGGGTACATGGCGGACGTTGAGAAACAAGATTCGAGG	1066
Db	1202	TTGTATCTTTCACAGTGTCTGGTTTACATGGCTGAGATGAGAAATGAAGATGTGTGAGG	1261
QY	1067	TTGGC--CTCGAAGGCCCTGACCTGGTGTTCATCGTGTATCCCGAGGCCATCGCCACCA	1123
Db	1262	TGGCCAAAGACGAGGTCCCGAGCCCTCTTTCATCAGTATGACGAAGCGATGACACCA	1321
QY	1124	TGACCGGCTCCGATCTGGGCGCATCATCTTCTTCCATGCTATTAACCTGGGACTTG	1183
Db	1322	TGCCAGCGTCCATCTTCTTGGCCATCATCTTCTTGTGATGTATATACGCTGGGCTTGG	1381
QY	1184	ACAGTACTTTTGGAGGCTTGGAGCGATCACACGCGCTTCTTGGACGAATATCCTCGAG	1243
Db	1382	ACAGCATTTTGGAGGCTTGGAGGGGATGATCAACGCTGTGCTGATGATGCCACAG	1441
QY	1244	TGTTAGCAGACATCCCGAAGTATTGTGGCTGTACTGCTTCTTATATATTGCG	1303
Db	1442	TCTGGCCCAAGCGCCCGGAGCGGCTGCTCGCCGGTGCATACCGCTTCTTTGGAT	1501
QY	1304	CTCTGCCCAACACATACGAGGTGTATACCTGTAAGACCTGTAAGTATGATGGCC	1363
Db	1502	CCCTGTCTACCTCTGACTTTTGGAGGGGCTTACGTGTGTAAGCTCTGAGAGATATGCCA	1561
QY	1364	CTGATTTGGCGATTCTATTTCGTGTATTGTCTGAGGCTGCCGCGTGTCTGGGTATG	1423
Db	1562	CGGGGCCCCAGTGTCTACTGTGCGCTGTATCGAAGACGATGCTGTGCTTGTCTATG	1621
QY	1424	GCGTGAACCGGCTCTGAAAGATGATGAGACACATGCTGGGCGACACCCCTGATGGTCT	1483
Db	1622	GCATCACTAGTTCTTGCAGGAGCGTGAAGAAATGCTGTGGCTTATAGCCGGGCTGTTCT	1681
QY	1484	GGAGGACCTGTTTGGTTCATCATCACTGTCCTTATCTTCTGCTGTCTGTTCTCGG	1543
Db	1682	GGAGGATCTGTGGGGTGGCCATCAGCCCTGTCTTCCCTTATCATATTGCAAGTTTC	1741
QY	1544	TTCTGGCACAGAGAGATGCTCGCGGGGAATACACTTATCCTCATGTCTATCACCG	1603
Db	1742	TGATAGCCCGCCACACTACGACTTTTCCAAATAATATTACTTACTGAGTACACT	1801
QY	1604	TAGCGGGGTGATGACCGGACACCGCTCTGCTGATCTTCCCTTATCATTTATTCAAAC	1663
Db	1802	TGGGTTACTGCATAGAACCTCATCTTTTCAATTGTGCATCCACATATATACCTTATCGGT	1861
QY	1664	TGCTCATCTCCTCGGCATTTGCATCAACCGCATCAAGACAA	1705
Db	1862	TGATCATCACTCCAGGACATTTAAMAGCGTATTATTAA	1903
RESULT 7			
US-10-219-051B-13970			
: Sequence 13970, Application US/10219051B			
: GENERAL INFORMATION:			
: APPLICANT: The General Hospital Corporation doing business as Massachusetts General			
: APPLICANT: Hospital / Bayer AG			
: TITLE OF INVENTION: Nucleotide sequences involved in pain			
: FILE REFERENCE: Lea 35693 Foreign Countries			
: CURRENT FILING DATE: 2003-05-09			
: PRIOR APPLICATION NUMBER: US 60/312,147			
: PRIOR FILING DATE: 2001-08-14			
: PRIOR APPLICATION NUMBER: US 60/346,382			
: PRIOR FILING DATE: 2001-11-01			
: PRIOR APPLICATION NUMBER: US 60/333,347			
: PRIOR FILING DATE: 2001-11-26			
: NUMBER OF SEQ ID NOS: 14715			

:	SOFTWARE:	perl script
:	SER ID NO	13970
:	LENGTH:	2508
:	TYPE:	DNA
:	ORGANISM:	Homo sapiens
:	PUBLICATION INFORMATION:	
:	DATABASE ACCESSION NUMBER:	EMBL / L05568
:	DATABASE ENTRY DATE:	2000-03-04
:	US-10-219-051B-13970	

  

Query Match	31.3%	Score 552.4;	DB 15;	Length 2508;
Best Local Similarity	59.5%;	Pred. No. 2,6e-157;		
Matches 953;	Conservative 0;	Mismatches 646;	Indels 3;	Gaps 1;

  

OY	107	GGCAGCGCCGACCTGTGGGCCAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGATTTCCAG	166
Db	302	GGAGCGGGGAACCTGTGGGCAAGAAGGTGGATTCTCTCATGTGATTTGGCTATGCTG	361
OY	167	TGATCTTGTGAACGTGTGGCGATTCCCTCATCTGTATTACAAATAGAGCGGTGGCT	226
Db	362	TGACACTGGGCAATGTCTGGCGCTTCCCCTCATATGTTACCAGATAGAGGGGGGCAT	421
OY	227	TCTGATCCGCTACTGCGTTATGCTGCTGTTTGGCGGGCTCCGCTGTTCTTCTCGAAC	286
Db	422	TCTCTCTCCCTACACCATCATGGCCATTTTTTGGGGGAATCCCTCTTTTACATGGAGC	481
OY	287	TGGCGTGGGCGACGTACACCGCGTGGCGCTCCCTCACCTCTGTGGAAACGGATTCGCCG	346
Db	482	TGCGACTGTGGACATACCAACCGAATGATGATCATTTCAATATGGAGAAAATCTGCCCCA	541
OY	347	CGCTTAAGAGTGTGCGGCTATGCCATCTGCATGATCGACATCTACATGGGCAATGACA	406
Db	542	TTTTTCAAAGGATTTGGTTATSCATCTGCATCATATGGCTTTTACATTTCTTCTCTACA	601
OY	407	ACAGATCATGGATGGCGGGGTGATTAACCTGATTCGTTCTCTGCGCTATTAACCTGTG	466
Db	602	ACACATCATGAGCTGTGGCGCTATTAACCTCATCTCTCTCTTACGAGCACGCTGCCCT	661
OY	467	TGCTGCCATGAGCAGCTGGCGCACACAGATGAGAACACGCCCTGTGCAGCGCGGTACCT	526
Db	662	GGACCAAGTGGCAAGACCTCTGSAACACTGGSCAACTGCAACAATTACTTCTCCGAGAGCA	721
OY	527	CACCTCAGACTAATCTTACTCTTCTTACACCGCGGAGAGATTTCTTGACACGTAAATGTAT	586
Db	722	ACATCACCTGAGACCTCCATTTCCACAGTCCCTCGTGAAGAAATTTTACACGGGCCACGCTC	781
OY	587	TGAGACGACACAAGCTATAACGGCTCGATGTAGCATAGGGCCGATCAAGCGCGTGGCTGC	646
Db	782	TGCAGATCCACGGGTCTTAAGGGGCTCCAGAGACCTBGGGGGATCAGCTGGCAGCTGCC	841
OY	647	TGTTGTGTTCGGGGCTTTTGTCTCTGTCTACTTCTCTTGTGGAAAGAGATCAGAGTGG	706
Db	842	TCTCATCATCTGATCTTCACTGTATTACTTCACTTCACTGATCTGGAAGAGCGCTCAAGACT	901
OY	707	CTGGCAAGGTGTGTGGGTGACACTCTGCGCCCGTAGTGAGTGCTGTGATTTCTGCTGG	766
Db	902	CTGGCAAGGTGTGTGGGTGACACTCTGCGCCCGTAGTGATTTCACTTCTTCTGCTGG	961
OY	767	CGAAGGCGTACACCTTCTCCAGAGACGAGGAGGGGATACGCTACTACCTTACCCAGAGT	826
Db	962	TGAAGGGGTGACACCTCCCTGGAGGCTGGAAGGGGGTCTCTTCTACTTTGAACCCAAAT	1021
OY	827	GGCACAATTTCCAATACTTAAGTATGATTTGACGGCGCATCCACAGATTTTCTTCTGC	886
Db	1022	GGCAGAAAATCTCTGGAGACAGGGGTGTGGATATGACAGCCGCTCAGATCTTCTTCTC	1081
OY	887	TGCGTCCCGGTTTGGGAACCTTACGCGGCTCTCCAGACTTACAACAAGTTTCAAACAACAT	946
Db	1082	TTGGTCCCGGCTTTGGGGTCTCTGCTGCTTTTGTCTAGCTATACAAAGATTCAACAACACT	1141
OY	947	GCTACAGGAGCGCGCTATCATCTTCTTATCAACTGCTTGACAGCACTTCTTCTGCTGTT	1006
Db	1142	GCTACAGGAGCGCGCTTGTGACAGCGGTGTGAGTGCATGATACAGAGCTTCTTCTGCGAT	1201



OY	1007	TCGTCATTTTCGCGTTTTGGGGATGACATGGGGGACGTTCCACAAAGACATCGAGAGG	1066
Db	1202	TTGTCATCTTTTACATGCTCGGTTTACATGGCTGAGATGAGAAATGAGATGTGTCGAGG	1261
OY	1067	TTGGC--CTCGAAGGCCCTTGAGCTGGTGTTCATCGTGTACCCCGAGGCAATCGCACCA	1123
OY	1184	ACAGTACTTTTGGAGGCTTGAGGCAAGCACACGAGGCTTTGGAGCAATATCTGAG	1243
Db	1382	ACACACAGCTTTGCAAGCTTGGAGGGGGTGATCGAGGCTGTCTGGATGATGCCACACG	1441
OY	1244	TGTTAGCGAGACATCGCGAAGTATTGTCGCTACTGCTTCTGTATCTATATTTGCG	1303
OY	1442	TCGTGGGCCAAGCGCGGGAGCGGTTGCGTCTGGCGGTGTCATCACCTGCTTTTGAT	1501
Db	1304	CTCTGCCACACACACATACGCTGTGTATACCTCGTAGACCTTACTANTGTATGGCC	1363
Db	1502	CCCTGGTGCACCCCTACTTTTGGAGGGGCTTACGTGTGAAGCTCTGGAGGAGTATGCCA	1561
OY	1364	CTGATATTGGCATTCTTATTCGTGTGATTTTGGATTTTGGAGGCTGGGGGTGGCTGGGTATG	1423
Db	1562	CGGGGGCCCGCAGTGTCTACTGTCTCGCGTGAATCGAAGCAGTGTGTGTCTTTGTTATG	1621
OY	1424	GCCTCGAACCCTCTCTGAAAGATGTGAGAGCAATGCTGGGGCACACCCCTGGATGTTCT	1483
Db	1622	GCATCACCTCACTGTCTGACAGGGACGTGAAGAAATGCTCGGCTTACGCCCGGGGTGCT	1681
OY	1484	GGAGGACCTGTGTGTCTTACATCACTGCTCCGATTTCTGTGTGTGTGTGTGTGTGTGTGT	1543
Db	1682	GGAGGATCTGT	1741
OY	1544	TTTCGGCACACAGAGAGATGCTCGGGGGAATACACCTATCCCTCATGTCTATCACCG	1603
Db	1742	TGATGAGCGCCGCCACAACTACGACTTTTCCAAATTAATTAATTCCTTACTGAGATATCACT	1801
OY	1604	TAGCTGGGTGATGATACCGGCACACCGCTCTCGTCATCTCTTTTACATTAATTCACAAAC	1663
Db	1802	TGGGTTACTGCTATGGAACCTCATCTTTTCATTTGCAATCCCAATATATACCTATCGGT	1861
OY	1664	TGCTCATCATCTCGTGGCAATGCAATCAACGCAATCAAGACAA	1705
	1862	TGATCATCATCTCCAGGACATTTTAAAGCGCTATTATTATAA	1903
RESULT 8			
PCT-US02-39565-43			
Sequence 43, Application PC/TUS0239565			
GENERAL INFORMATION:			
APPLICANT: INCYTE GENOMICS, INC.			
APPLICANT: BAUGHN, Mariah R.			
APPLICANT: CHANG, Hsin-Ru			
APPLICANT: CHIEN, David			
APPLICANT: DUGGAN, Brendan M.			
APPLICANT: EMERLING, Brooke M.			
APPLICANT: GORVAD, Ann E.			
APPLICANT: GRIFFIN, Jennifer A.			
APPLICANT: HAFALIA, April J.A.			
APPLICANT: HAWKINS, Philip R.			
APPLICANT: JACKSON, Alan P.			
APPLICANT: JIANG, Xin			
APPLICANT: JIN, Pei			
APPLICANT: KABLE, Amy E.			
APPLICANT: KHARE, Reena			
APPLICANT: LAL, Preeti G.			
APPLICANT: LEE, Ernestine A.			
APPLICANT: LEE, Sally			
APPLICANT: LEE, Soo Yeun			

```

APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: REDDY, Roopa
APPLICANT: RICHARDSON, Thomas W.
APPLICANT: RING, Huijun Z.
APPLICANT: SPRAGUE, William W.
APPLICANT: SWARNAKR, Anita
APPLICANT: TANG, Y. Tom
APPLICANT: ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: PF-1336 PCT
CURRENT APPLICATION NUMBER: PCT/US02/39565
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/340,741
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/351,359
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/359,506
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PERL Program
SEQ ID NO 43
LENGTH: 2770
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7508471CB1
PCT-US02-39565-43

```

query Match	31.38;	Score 552.4;	DB 2;	Length 2770;
Best Local Similarity	59.58;	Pred. No. 2.8e+157;		
Matches 953;	Conservative 0;	Mismatches 646;	Indels 3;	Gaps 1

QY	107	GGCAGGCGGACACCTGGGCGCAAGAAAGGACAGAGTTCTCGTGGCGGGGATGGGATTTGGCAG	166
Db	552	GGGAACGGGAGACCTGGGGGCAAGAAAGGATTTCTTCTCTCAGTATGGCTATGCTG	611
QY	167	TGGATCTTGGTAACGTGTGGCGGATTTCCCTACATCTGTATACCAAGATGAGCGGTGCGT	226
Db	612	TGGACCTGGGCATMTCTGGCGGCTTCCCTCATATATGTTACCAAGAAATGAGGGGGGCGAT	671
QY	227	TGCTGATCCCGTACGCGCTTATGCTGCTGTGTTGGCGGGGTCGGCGGTCTTCTCTCTGGAC	286
Db	672	TGCTCTCTCCCTACACATCATGCGCATTTTGTGGGGGAATTCGCGCTTTTACATGGAAC	731
QY	287	TGGCGCTGGGCGAGTACCACCGCGTGGCGGCTCGTCACCTCTCTGCGAAAGGATGTGGCCGG	346
Db	732	TGGCACTGGGACAGTACCAACCGGAATGGATGCAATTTCAATATGGAGAAATATGCCCCA	791
QY	347	GCGTTAAAGTGTCGGCTATGCCATCTGCATGATGCATCTCATGAGGAGTACTACCA	406
Db	792	TTTTCAAAAGGATGGTATGTCATCTGCATCTGATCTTATGCTTTACATGTCTCTACTACA	851
QY	407	AACAGCATATCGGATGGCGGGTGTATTAACGTGATCGCTTCTTCGGGTCTATTAACCTCG	466
Db	852	ACACCATATGCGCTGGGCGGCTATACACCTCATCTCTCTTCACGAGCAAGCTGCCCT	911
QY	467	TGCTGATGAGCAACGCTGGCAACAAGATGGGAACAGCGCGCTGCGACGCGGTCACCT	526
Db	912	GGACCAAGCTGCAGAAGACTCTGGAGACACTGGCAACCTGCACCAATTACTTCTCCGAGGACA	971
QY	527	CACCTCAGACTAATCTTAACCTTCTACACCGGCGGAAGAGTTCTTGAGACGTAATGTAT	586
Db	972	ACATCAGCTGAGACCTTCATTTCCAGAGTCCCTGCTGTAAGAAATTTTACAGCGCGCACGTCC	1033
QY	587	TGGAGCAGACAGTCTTAACGGCTGGATGACATGGGGCGGATCAAGCGGTGCTGGCTC	646
Db	1032	TGCACATCAGCAGCGGTCTAAGGGGCTCCAGAGACCTGGGGGCGCATCACACTGGCAGCTTGGCCC	1091
QY	647	TGTGTGTGTGGGGGCTTTTGTCTCTCGTCACTCTCTCTGTGGAAAGAGATCAGGAGTG	706
Db	1092	TCTGGATCATGCTGATCTTTCACGTGTATCTTAATTCACACATCTGGAAAGGCGTCAAGACCT	1155



707 CTGGCAAGGTGTGGTGTGACAGCTGTGCCCCCTAGCTGTGCTGTATCTGTCTGG 766  
1152 CTGGCAAGGTGTGGTGTGACAGCTGTGCCCCCTAGCTGTGCTGTATCTGTCTGG 1211  
767 CGAAGAGGTGTGACAGCTGTGCCCCCTAGCTGTGCTGTATCTGTCTGG 826  
1212 TGAGGGGTGTGACAGCTGTGCCCCCTAGCTGTGCTGTATCTGTCTGG 1271  
827 GGCACAAATTTGCAAACTCTAAGTATGATGTGAGGGGCAATCCAGATTTCTCTGCG 886  
1272 GGCACAAATTTGCAAACTCTAAGTATGATGTGAGGGGCAATCCAGATTTCTCTGCG 1331  
887 TCGGTCCTGCTGTGAG 946  
1332 TTGGTCCTGCTGTGAG 1391  
947 GCTACAGGAG 1006  
1392 GCTACAGGAG 1451  
1007 TCGTATTTCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1066  
1452 TTGTCATCTTACAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1511  
1067 TTGGC---CTGAG 1123  
1512 TGAGCAAG 1571  
1124 TGACCGGCTCGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1183  
1572 TGCCAGGCTCGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1631  
1184 ACAGTATCTTGTGAG 1243  
1632 ACAGTATCTTGTGAG 1691  
1244 TGTGAG 1303  
1692 TGTGAG 1751  
1304 CTCTGAG 1363  
1752 CCTGAG 1811  
1364 CTGATGAG 1423  
1812 CGGGGAG 1871  
1424 GCGTGTGAG 1483  
1872 GCATCAGTGTGAG 1931  
1484 GAG 1543  
1932 GAG 1991  
1544 TTTGAG 1603  
1992 TGATGAG 2051  
1604 TAGGCTGTGAG 1663  
2052 TGGGTGTGAG 2111  
1664 TGCTATCAGTGTGAG 1705  
2112 TGATCATCATCTGAG 2153

RESULT 9  
US-09-949-016-3430  
; Sequence 3430, Application US/09949016  
; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows version 4.0  
SEQ ID NO: 3430  
LENGTH: 2964  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-3430

Query Match 31.3%; Score 552.4; DB 11; Length 2964;  
Best Local Similarity 59.5%; Pred. No. 2.9e-157;  
Matches 953; Conservative 0; Mismatches 646; Indels 3; Gaps 1;

107 GGCAGCGGAGACCTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 166  
302 GGGAGCGGAGACCTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361  
167 TGATCTTGTGTAACGTGTGGGAGATTCCTTACATCTGTATCCAGATGAGAGAGAGAGAG 226  
362 TGACCTGGGAGAGATGTGGGAGATTCCTTACATCTGTATCCAGATGAGAGAGAGAGAG 421  
227 TCCATATCCGAGTGTGAG 286  
422 TCCATATCCGAGTGTGAG 481  
287 TGGGCTGGGAG 346  
482 TGGGCTGGGAG 541  
347 GCGTAAAGAGTGTGGGAGATTCCTTACATCTGTATCCAGATGAGAGAGAGAGAGAGAG 406  
542 TTTTAAAGAGTGTGGGAGATTCCTTACATCTGTATCCAGATGAGAGAGAGAGAGAGAG 601  
407 ACACATCATCGAGATGGGAG 466  
602 ACACATCATCGAGATGGGAG 661  
467 TGTGCTGAG 526  
662 GAGCAGAGTGTGAG 721  
527 CACCTGAGAGTGTGAG 586  
722 ACATACCTGTGAG 781  
587 TGGAG 646  
782 TGACATCATCGAGATGGGAGAGATTCCTTACATCTGTATCCAGATGAGAGAGAGAGAGAG 841  
647 TGTGCTGAG 706  
842 TGTGCTGAG 901  
707 CTGGCAAGGTGTGGTGTGACAGCTGTGCCCCCTAGCTGTGCTGTATCTGTCTGG 766  
902 CTGGCAAGGTGTGGTGTGACAGCTGTGCCCCCTAGCTGTGCTGTATCTGTCTGG 961  
767 CGAAGAGGTGTGACAGCTGTGCCCCCTAGCTGTGCTGTATCTGTCTGG 826  
962 TGAGGGGTGTGACAGCTGTGCCCCCTAGCTGTGCTGTATCTGTCTGG 1021  
827 GGCACAAATTTGCAAACTCTAAGTATGATGTGAGGGGCAATCCAGATTTCTCTGCG 886

```

Db      1022 GGCAGAAACTCTGGAGACAGGGGCTGTGATGATGACGCCCTCAGATCTCTCTC 1081
Qy      887 TCGTCCCGGGTTCGGGAACCTACTGGGCTCTCCAGCTACACAAAGTTCAACACACT 946
Db      1082 TTGGTCCGGGCTTTGGGCTCTGCTTTGATGCTACAAAGTTCAACAACT 1141
Qy      947 GCTACAGGAGCGGCTCATCTTCTTATCACTGTGACAGCTTCTCTGTGTT 1006
Db      1142 GCTACCAAGATGCCCTGGTGACACCGCTGTGAACATGTCATGACGCTTCTGTGGAT 1201
Qy      1007 TCGTCAATTTCTCGGTTTGGGTCATGCGCAGCTTCAGAACAAAGACATGAGAG 1066
Db      1202 TTGTATCTTCACTGCTCGGTTACATGGCTGAGATGAGATGAATGATGCTGAG 1261
Qy      1067 TTGGC---CTGGAAGCCCTGACGCTGTGCTCATGCTGTACGCCCAAGCCACCA 1123
Db      1262 TGGCCAAAGACGAGCTCCACGCTCTCTCATCAGTATGCAAGGATGAGCA 1321
Qy      1124 TGACCGGCTCGTCTTGGGCTCATCTTCTCTCATGCTTATACCTGGGACTTG 1183
Db      1322 TGCCAGCGCTCCACTTCTTGGCATCTTCTTCTATGATATCAACGCTGGCTTG 1381
Qy      1184 ACAGTACTTTGGAGGCTTGGAGCAATCACCGGCTTGGCAGCAATATCTCGAG 1243
Db      1382 ACAGCAGCTTTGCAAGGCTTGAGGGGATGATCAGCGCTGCTGATGATGCCACAG 1441
Qy      1244 TGTGAGGAGACATGCGGAGTATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
Db      1442 TGTGGGCAAGCGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501
Qy      1304 CTCTGCCACACACACATACGCTGTGATATACCTGTAGACCTACTCATATGTATG 1363
Db      1502 CCTGTGACCTGCTGCTTGTGGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1561
Qy      1364 CTGATTTGGGCTTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
Db      1562 CGGGGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1621
Qy      1424 GGTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
Db      1622 GCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1681
Qy      1484 GAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1543
Db      1682 GAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
Qy      1544 TTCTGCAACAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1603
Db      1742 TGATGAGCGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801
Qy      1604 TAGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1663
Db      1802 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1861
Qy      1664 TGTCTCATCTCTCTGCAATTTGATCAACCGCATCAAGCA 1705
Db      1862 TGATCATCTCTCCAGGACATTTAAAGCGTATTTAA 1903

```

```

; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-38741
Query Match 31.3%; Score 552.4; DB 15; Length 2964;
Best Local Similarity 59.5%; Pred. No. 2.9e-157;
Matches 953; Conservative 0; Mismatches 646; Indels 3; Gaps 1;

Qy      107 GGCAGCGGACACCGCGGCGCAAGAGGAGGATTCCTGCTGGGCTGGGATTCGAG 166
Db      302 GGAAGCGGAGACCTGGGGCAAGAGGTGATTTCTCTCTCACTGATTTGGCTATGCTG 361
Qy      167 TGGATCTTGTAACGCTGTGGGATTCCTCATATCTGTTACCAAGATGAGGCGGTGCT 226
Db      362 TGGACCTGGCAATGTGGCGCTTCCCTCATATGTTACCAAGATGAGGCGGCGAT 421
Qy      227 TCTCATCCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 286
Db      422 TCTCTCTCCCTACACCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
Qy      287 TGGGCGTGGGCGAGTACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 346
Db      482 TCGCACTGGAGAGTACACCGCAAAATGATGATTTCAATATGAGGAAATCTGCCGA 541
Qy      347 CGCTTAAAGGTGTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 406
Db      542 TTTTCAAGGATGTGTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 601
Qy      407 ACAGATATGATGATGGGCGGTATTTACCTGATGCTTCTGCTGCTTAACTGTG 466
Db      602 ACACCATATGCTGCGGCGGTATTTACCTGATGCTTCTGCTGCTGCTGCTGCTGCT 661
Qy      467 TGTCTGCAAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
Db      662 GGACCACTGCAAGAGTCTGGAACACTGGAACACTGGAACACTGGAACACTGGAACACT 721
Qy      527 CACTCAGACTAATCTACTTCTTACACCGGCGCAAGAGTCTTGAACGATATGAT 586
Db      722 ACATCACTGCACTCTCATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
Qy      587 TGGACACACAGCTCTAAGCGCTGATGATGATGATGATGATGATGATGATGATGAT 646
Db      782 TGCATATCACCGGCTAAGGCGCTGCAAGAGCTGAGGCGGATGCTGGAAGCTGCGCC 841
Qy      647 TGTGCTGCTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
Db      842 TCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 901
Qy      707 CTGCAAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 766
Db      902 CTGCAAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
Qy      767 CGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 826
Db      962 TGAAGGCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1021
Qy      827 GGCACAAATGCAAACTCTAAGGATGATGATGATGATGATGATGATGATGATGAT 886
Db      1022 GGCAGAAACTCTGAGACAGGGGCTGTGATGATGACCGCGCTGATGATCTTCTCTC 1081
Qy      887 TCGTCCCGGGTTCGGAAACCTACTGGGCTCTCCAGCTACACAAAGTTCAACAACT 946
Db      1082 TTGGTCCGGGCTTTGGGCTCTGCTTTTGGATGCTACAAAGTTCAACAACT 1141
Qy      947 GCTACAGGAGCGGCTCATCTTCTTATCACTGTGACAGCTTCTCTGTGTT 1006
Db      1142 GCTACCAAGATGCCCTGGTGACACCGCTGTGAACATGTCATGACGCTTCTGTGGAT 1201
Qy      1007 TCGTCAATTTCTCGGTTTGGGTCATGCGCAGCTTCAGAACAAAGACATGAGAG 1066
Db      1202 TTGTATCTTCACTGCTCGGTTACATGGCTGAGATGAGATGAATGATGCTGAG 1261
Qy      1067 TTGGC---CTGGAAGCCCTGACGCTGTGCTCATGCTGTACGCCCAAGCCACCA 1123

```

Db 1262 TGGCCAAAGACGACGATCCACGCTCCTTCATCATGATGACAGAGATAGCCAA 1321  
OY 1124 TGACCGGCTCCGCTGTTCTGGCCATCATCTTCTCTCATGCTTATTAACCTGGACATTG 1183  
Db 1322 TGCCAGCGCTCCCTTCTTCTTGGCCATCTTCTTCTGATTTAAATCAACGCTGGCGTTG 1381  
OY 1184 ACAGTACTTGGAGCTTGGAGGACGATCACCAGGCTTTGGCGCAATATCCGCGAG 1243  
Db 1382 ACAGACGCTTTCAGAGCTTGGAGGGGATGATACGCGCTGCTGATGAGTCCACACG 1441  
OY 1244 TGTAGGACGACATGCGAAGTATTTGCTGCTACTGCTTCGTTTCATATTAATTTGCG 1303  
Db 1442 TCTGGGCGCAAGCGCGGAGCGGTTGCTGCTGCGCGTGTGATCAACCTGCTCTTTGGAT 1501  
OY 1304 CTCTGCGCCACACACATACGCTGCTGATTAACCTGCTAGACCTACTCAATGTTGATGCC 1363  
Db 1502 CCTGCTGCTACCTGATTTTGGAGGGGCTTACGCTGCTGAAGCTGCTGAGGATAGCCA 1561  
OY 1364 CTGATTTGGGCTATTTCTATGCTGATTTGCTGAGGCTCGGCGGCTGCTGGGCTGATG 1423  
Db 1562 CGGGGCGCGCATGCTGCTACTGCTGCGCTGATGAGACATGCTGCTGCTTGGTTTATG 1621  
OY 1424 GCGTGACCGGCTTCTGTAAGATGTAGAGACATGCTGGGCAACCCCTGGATGCTCT 1483  
Db 1622 GCATCACTGATTTCTGACGAGCGTGAAGAAATGCTGCGCTTACAGCCGCGGCTGCTCT 1681  
OY 1484 GGAGACCTGTTGCTTCTGATCATGCTCCGCTATTTCTGCTGCTGCTGCTGCTGCTGCT 1543  
Db 1682 GGAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741  
OY 1544 TTTCTGACACAGAGATGCTGCGGGGGAATACACTATCCGCTGATGCTGATACCGG 1603  
Db 1742 TGATGAGCGCGGACACACTACACTTTTCCATATATATATATCTTACTGAGTATATCT 1801  
OY 1604 TAGGCTGGTGTATGACCGGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1663  
Db 1802 TGGGTTACTGATGAGAACCTCATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1861  
OY 1664 TGGCTATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1705  
Db 1862 TGATCATCACTCCAGGACATTTAAAGACGCTATTTATTA 1903

RESULT 11  
US-60-453-135-1580  
Sequence 1580, Application US/60453135  
GENERAL INFORMATION:  
APPLICANT: CARLILL, Michele  
APPLICANT: IAKOUBOVA, Olga  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CL001456  
CURRENT APPLICATION NUMBER: US/60/453,135  
CURRENT FILING DATE: 2003-03-10  
NUMBER OF SEQ ID NOS: 82762  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1580  
LENGTH: 2342  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-453-135-1580

Query Match 29.7% Score 524; DB 18; Length 2342;  
Best Local Similarity 59.4%; P-Id. No. 1,2e-148;  
Matches 948; Conservative 12; Mismatches 612; Indels 24; Gaps 4;

OY 103 GCGCGACGACGACGACGCTGGGCGAAGAGGACAGAGTCTGCTGGCGGTGGGATTC 162  
Db 412 GCGCAGCCCGGAGAGCTGGGCGAAGAGATGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471  
OY 163 GCAGTGAATCTTGTAACTGTGGGATTTCCCTTACATCTGTTACAGAAATGAGGCGGT 222

Db 472 GCAGTGAACCTGGCCACGCTGGGCGCTTCCCTTACTCTGCTTACAGAAAGGCGGCGT 531  
OY 223 GCGTTCCTGATCCCTTACCTGCTTATGCTGCTGCTTGGGCGGCTCCGCTGCTTCTGCTG 282  
Db 532 GCGTTCCTGATCCCTTACCTGCTTATGCTGCTGCTTGGGCGGCTCCGCTGCTTCTGCTG 591  
OY 283 GAACCTGGCGCTGGGCGACGACGACGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 342  
Db 592 GAGCTGCTGCTGGGACAGTACAGAACCGGAGGAGGCGCTGCGACCGCTTGGAAA--ATCTGCG 648  
OY 403 TACAAACGATCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450  
Db 709 TACAAACGATCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768  
OY 451 GCGTATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509  
Db 769 CCTGAGCGACGATGCTGCGACACGCTGAGACGACCCCACTGATACCGACCCCAAGCTCTGCG 828  
OY 510 -----GTGACGCGCGGTACCTTACCTGATTAATCTTACTCTTCTTACACCGCGGAG 564  
Db 829 AATGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888  
OY 565 GAGTTCCTGACGATTAATGATTTGGAGCAGCAGACAGTCTAACGGCTGATGATGATGATG 624  
Db 889 GAGTTCCTGACGATTAATGATTTGGAGCAGCAGACAGTCTAACGGCTGATGATGATGATG 948  
OY 625 CGATCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 684  
Db 949 CTGCGCCAGTGGCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008  
OY 685 TTTGTGAAGAAGTACAGAGTCTGCGAAGTGTGTGGTGAACAGCTTGCGCCCGTAC 744  
Db 1009 CTCTGGAAGAAGGCTGGAACATCAGAAAGGCTGTGATGATGATGATGATGATGATGATG 1068  
OY 745 GTGCT 804  
Db 1069 TTTGCT 1128  
OY 805 CGCTACTACTTACCCAGAGTGGCAGAAATTTGCAAACTTAAGTATGATGATGATGATGATG 864  
Db 1129 AATGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188  
OY 865 GCATCCAGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 924  
Db 1189 GCAACTCAGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248  
OY 925 TACAAACATTTGCAAACTGCTTACAGGAGCGGCTGATGATGATGATGATGATGATGATGATG 984  
Db 1249 TACAAACATTTGCAAACTGCTTACAGGAGCGGCTGATGATGATGATGATGATGATGATGATG 1308  
OY 985 TTTGACGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044  
Db 1309 ATCAGCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1368  
OY 1045 CAGAACAGATGATGAGAGGTTGGCTGGAAGGCTTGGAGCTGATGATGATGATGATGATGATG 1104  
Db 1369 CAGAACAGATGATGAGAGGTTGGCTGGAAGGCTTGGAGCTGATGATGATGATGATGATGATGATG 1428  
OY 1105 CCGAGGCGATGCGCCATGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164  
Db 1429 CCGAGGCGATGCGCCATGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1488  
OY 1165 CTTATTAACCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1224  
Db 1489 CTCTGCGCGCTGCGCTTGGACACTCAATGAGAGGATGAGAGGCTTCAATCAGCGGCTGCG 1548  
OY 1225 TCGCAGCAATATCTGAGTGTAGCGACATGCGGAAGTATTTGCTGCTGCTGCTGCTGCTGCTGCT 1284  
Db 1549 GCAGATGAGCT---TTCAGGTCTGGAAGCAGACCGGAACCTTTCACATTTGCTGCTGCTGCTGCT 1605









```

: APPLICANT: The General Hospital Corporation doing business as Massachusetts General
: APPLICANT: Hospital / Bayer AG
: TITLE OF INVENTION: Nucleotide sequences involved in pain
: FILE REFERENCE: Lea 35693 Foreign Countries
: CURRENT APPLICATION NUMBER: US/10/219,051B
: PRIOR FILING DATE: 2003-05-09
: PRIOR APPLICATION NUMBER: US 60/312,147
: PRIOR FILING DATE: 2001-08-14
: PRIOR APPLICATION NUMBER: US 60/346,382
: PRIOR FILING DATE: 2001-11-01
: PRIOR APPLICATION NUMBER: US 60/333,347
: PRIOR FILING DATE: 2001-11-26
: NUMBER OF SEQ ID NOS: 14715
: SOFTWARE: Perl script
: SEQ ID NO 10901
: LENGTH: 1983
: TYPE: DNA
: ORGANISM: Homo sapiens
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: EMBL / M65105
: DATABASE ENTRY DATE: 2000-03-04
: 10-219-051B-10901

```

```

Query Match      29.6%; Score 522.4; DB 15; Length 1983;
Best Local Similarity 59.9%; Pred. No. 3,5e-148;
Matches 956; Conservative 0; Mismatches 616; Indels 24; Gaps 4;

```

```

QY 103 GGGCGGACCGCGAGACCTGGGCGAGAGAGGAGAGAGTTCCTGCTGGCGGTGGTGGATTC 162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 217 GGGCGGACCGCGAGACCTGGGCGAGAGAGGAGAGTTCCTGCTGGCGGTGGTGGATTC 276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 163 GCAGTGCATCTTGTATGCTGTGGCGATTCCTCCATCATCTGTATACAGATGGAGCGGT 222
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 277 GCAGTGCATCTTGTATGCTGTGGCGATTCCTCCATCATCTGTATACAGATGGAGCGGT 336
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 223 GGGTCTGTATCCCGTATGCTGTATGCTGTATGCTGTATGCTGTATGCTGTATGCTGTAT 282
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 337 GCGTCTGTATCCCGTATGCTGTATGCTGTATGCTGTATGCTGTATGCTGTATGCTGTAT 396
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 283 GAACGGGCGTGGGCGAGTACCAACCGCTGGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 342
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 397 GAGCTGGCTGTGGGCGAGTACCAACCGGAGGCGGTGCGCAACGTTGGAAA--ATCTGC 453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 343 CCCGCGCTTAAAGTGTGCGGTATGCCATGTGCATGTGCATGTGCATGTGCATGTGCATGTGC 402
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 454 CCATCTTAAAGGCGTGGTATGCTGTATGCTGTATGCTGTATGCTGTATGCTGTATGCTGTATG 513
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 403 TACACAGCATCATCGGATGGGCGGTGTATACCTGATCGCTTC-----TCTC 450
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 514 TACACAGCATCATCGGATGGGCGGTGTATACCTGATCGCTTC-----TCTC 573
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 451 GGGTCTATTAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 574 CCCTGGACCGACTGTGGCGACACCTGGAGCCGCCCACTGTACGACCCCAAGCTCTTC 633
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 510 -----GTGCAGCCCGGTGCTACCTGCTACCTGCTACCTGCTACCTGCTACCTGCTACCTG 564
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 634 AATGGCTCGTGTGTGGCAACCAACCAAGTACTCCAAAGTACAGGCGCGAGGC 693
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 565 GAGTCTTGAAGCATATATTTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 624
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 694 GAGTTTATAGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 625 CCGATCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 754 CTGCCCGCATGTGAGCTCTTGTGCTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 813
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 685 TTGTGGAAGAGATCAGAGATGTGTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 744
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 814 CTCTGGAAGAGATCAGAGATGTGTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 873
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 745 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 804
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

DB 874 TTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 933
QY 805 CCGTACTACTTACCCCAAGTGGGCAATTTGCAAACTCTAAGTATGATGATGACGG 864
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 934 AATGCCCTACCTGACATGACCTTCAACCTTGAAGAGCCACGGTATGATGTGTC 993
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 865 GCATCCGATTTTCTGCGCTGCGTCCGGTGGGATGGAACCTACTGGCGCTCCAC 924
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 994 GCACTCAGATATTTTTTTTCTGTTGGGGCTGATTTGGAGTATGATTTGCAATTTGCTGCT 1053
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 925 TACAAAGTTCACCAACTGCTACAGGAGCGCTCATCATCTTCTTCAACTGC 984
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1054 TACAAAGTTCACCAACTGCTACAGGAGCGCTCATCATCTTCTTCAACTGC 1113
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 985 TTGACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1044
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1114 ATCACAGGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1173
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1045 CAGAACAGAGCATGAGGAGTGGCTGCGAAGGCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 1104
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1174 CACAAAGTTCACCAACTGCTACAGGAGCGCTCATCATCTTCTTCAACTGC 1233
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1105 CCCGAGCCATGCGCCACATGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1164
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1234 CCAGAGGCCATTTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1293
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1165 CTATATCCCTGGGACTTACAGTACTTTTGAAGTCTTGAAGTACCAAGCTCTT 1224
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1294 CTCTGCGCTGCGCTTACAGCTCAATGGGAGGATGAGGCTGTCTATCACGGGCTG 1353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1225 TCGCAAGTATCTGAGTGTAGGACAGCATCGGAGATATTTGTGCTGCTGCTGCTGCTGCTGCTG 1284
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1354 GCAGATGACT---TCAGGCTCTGAAGCGACACCGGAACTCTTCAATTTGGCGTCAAC 1410
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1285 CTGTTCTATATATTTGCGCTGCTGCGCCACACCATATGAGTGTATACCTGTAGAC 1344
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1411 TTGAGCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1470
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1345 CTACTCAATGTATGCGCTGATTTGGGATTTCTATTTGCTGATTTGCTGAGCTGCG 1404
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1471 CTCTGAGACCTTTGCTGCTGCGGACCTCTCATCTTTTGTCTCTCATGAGGACATC 1530
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1405 GCGTGTGCTGCTGATGATGCGCTGCGACCGTCTCTGAGAGTGTAGGACATGCTGGGG 1464
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1531 GAGGTTTCTGCTGTTTATGAGTGTGAGAGTTCAGCAAGACATCCAGCAGATGATGGG 1590
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1465 CACACCCGTGATGTTCTGAGAGACCTGTGTCTTACATGATCCGATTTCTGCTG 1524
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1591 TTGAGGCGGGGTCTATAGTGAAGACTGTGCTGGAATGTGTCAGTCTGCTGCTGCTGCTG 1650
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1525 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1584
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1651 TTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1710
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1585 CCCTGAGTCTATACCTGAGGCTGAGTATGAGGAGGAGCCAGCTGCTGCTGCTGCTGCTGCTG 1644
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1711 CCGCCCTGGGCAACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1770
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1645 CTTCATTTATCTACAACCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1771 ATCTAGCTCATCTATAGTTCCACAGCAGCAGGCG 1806
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Search completed: July 18, 2003, 16:59:29  
 Job time : 1005 secs



